Amendments to the Specification:

Please replace the paragraph beginning on page 5, line 23 with the following amended paragraph:

According to the invention, this object is achieved by a protein having splicing factor activity in plants, which either

- comprises the amino acid sequence of the protein according to Fig. 1A of the appendix (SEQ ID NO:19), or
- comprises the sequence of the amino acids 1 to 4, 7 to 19, 45 to 52, 111 to 116, and 149 to 153 of the protein according to Fig. 1A (SEQ ID NO:19) of the appendix and has more than 85% similarity with this protein, or
- comprises more than 60% similarity with the splice proteins atSRp34/SR1 and SF2/ASF according to Fig. 2 of the appendix, wherein the G-rich sequence, which corresponds to the amino acids 85 to 113 of the atSRp34/SR1 (SEQ ID NO:22) protein is substituted by an S-rich sequence, or

corresponds to, or is derived from, the protein corresponding to Fig. 1A (SEQ ID NO:19) from a plant other than Arabidopsis thaliana.

Please replace the paragraph beginning on page 6, line 12 with the following amended paragraph:

The protein according to the invention advantageously is characterized in that it comprises the sequence of the amino acids 1 to 4, 7 to 19, 22 to 72, 74 to 85, 96 to 141, 149 to 153, 156 to 172, with amino acid 168 being variable, yet not D or N, of the protein according to Fig. 1A (SEQ ID NO: 19) of the appendix. The highly conserved sequences indicated preferably are arranged such that the distances between the sequences indicated approximately correspond to those according to Fig. 1A of the appendix, preferably not more than 5 amino acid deletions or amino acid insertions being provided. Particularly preferred are sequences in which either no, or merely one single, deletion or insertion is present between the conserved sequences.

Please replace the paragraph beginning on page 6, line 25 with the following amended paragraph:

The protein according to the invention may comprise one or more amino acid substitutions as compared to the protein illustrated in Fig. 1A of the appendix, as long as the sequence of the amino acids 1 to 4, 7 to 19, 45 to 52, 111 to 116, and 149 to 153 of the protein according to Fig. 1A (SEQ ID NO: 19) of the appendix or the function of the protein as splicing factor are not affected. Its function as a splicing factor is to be considered to be affected if the protein comprises, e.g., only 10 to 20% of the natural activity of the protein according to Fig. 1A of the appendix.

Please replace the paragraph beginning on page 7, line 14 with the following amended paragraph:

According to the invention, all proteins are preferred which comprise an amino acid sequence having at least 90% identity with the sequence of the amino acids 1 to 85 and 96 to 222 of the protein according to Fig. 1A (SEQ ID NO:19) of the appendix.

Please replace the paragraph beginning on page 7, line 19 with the following amended paragraph:

Proteins which comprise an amino acid sequence that has at least 95%, in particular at least 98%, identity with the sequence of the amino acids 1 to 85 and 96 to 222 of the protein according to Fig. 1A (SEQ ID NO:19) of the appendix are particularly preferred.

Please replace the paragraph beginning on page 8, line 4 with the following amended paragraph:

The S-rich sequence between amino acid 95 and 102 of the sequence according to Fig. 1A (SEQ ID NO:19) of the appendix preferably comprises at least 4, in particular at least 7, serine residues. Advantageously, it is G-free, in particular free from GGR or GGR repeats.

Please replace the paragraph beginning on page 8, line 9 with the following amended paragraph:

The protein according to the invention can be provided by standard methods of molecular biology also from other plants, because of the high homology of such proteins, such as by PCR coupled cloning methods or by other screening of gene libraries, e.g. with the sequence according to Fig. 1A (SEQ ID NO:19) of the appendix.

Please replace the paragraph beginning on page 8, line 15 with the following amended paragraph:

According to a further aspect, the present invention relates to nucleic acid molecules, which either

- comprise a nucleic acid sequence according to Fig. 1A of the appendix (SEQ ID NO:18), or
- comprise a nucleic acid sequence encoding a protein of the invention, or

comprise a nucleic acid sequence which, under stringent conditions, binds to the nucleic acid molecule according to Fig. 1A (SEQ ID NO:18) and encodes a splice protein active in plants or is complementary thereto.

Please replace the paragraph beginning on page 9, line 7 with the following amended paragraph:

In a further aspect, the invention moreover relates to a system comprising a nucleic acid which encodes a protein according to any one of the claims, and a nucleic acid which encodes

- the atSRp34/SR1 protein of Arabidopsis thaliana or
- the protein corresponding to Fig. 1A (SEQ ID NO:19) from a plant other than Arabidopsis thaliana, or
- a protein derived from these proteins,

wherein at least one of the nucleic acids is under the control of a promoter not naturally connected with these nucleic acids.

Please replace the paragraph beginning on page 17, line 11 with the following amended paragraph:

Analysis of alternatively spliced isoforms

RNA blot analyses were done as described (Lopato et al. 1996b). cDNAs encoding alternatively spliced isoforms were obtained by RT-PCR using total RNA preparations from A. thaliana plants at different stages of development and primers derived from the 3' untranslated region (for reverse transcription).

(1) 5'-AAATGAGCTCAAATGTATATGTATGGAAAAACC-3' (SEQ ID NO:1) (atSRp30) and

(2) 5'-AATGAGCTCGAAACGATATCTTCAAAAAAAAAC-3' (SEQ ID NO:2) (atSRp34/SR1)

(The underlined nucleotides correspond to restriction sites) and from the beginning of the 5' untranslated region at the end of coding region for (PCR):

(3) 5'-AAACTGGATCCAGAACAATCTAACGCTTTCTCG-3' (SEQ ID NO:3) (atSRp30) and

(4) 5'-ATATAGGATCCTCAACCAGAUAUCACAGGTG-3' (SEQ ID NO:4) (atSRp30); and

(5) 5'-AAATATCTAGAGATCTCAAATCGACGACC-3' (SEQ ID NO:5) (atSRp34/SR1) and

(6) 5'-ATATAGGATCCCATTTTACCTCGATGGAC-3' (SEQ ID NO:6) (atSRp34/SR1).

All products were sequenced. Alternative splicing of the long introns was studied using primers derived from adjacent exons:

(7) 5'-AATGAGCTCTGTGTCACCTGCTAGATCC-3' (SEQ ID NO:7) (atSRp30) and

(8) 5'-ATATAGGATCCAGATATCACAGGTGAAAC-3' (SEQ ID NO:8) (atSRp30); and

(9) 5'-ATAGGATCCAGGAGCAGAAGTCCCAAGGCAAAG-3' (SEQ ID NO:9) (atSRp34/SR1) and

(10) 5'-AAAGTCGACAGAAGGTAGAGGAGATCTTGATC-3' (SEQ ID NO:10) (atSRp34/SR1).

Please replace the paragraph beginning on page 18, line 15 with the following amended paragraph:

Constructs for promoter analysis and overexpression

Approximately 1 kb of promoter sequences of atSRp30 and atSRp34/SR1 plus their complete 5' untranslated regions (including the first intron in the case of atSRp34/SR1) were obtained by PCR from genomic clone GatSRp30 and genomic DNA of A. thaliana, respectively, as a template, using primers

(11) 5'-AAACTAAGCTTGGTATCTTCTTCCCTGCAAG-3' (SEQ ID NO: 11) (atSRp30);

(12) 5'-AAACCTAGGCGGCTACTCAGCTGATACCTCAGAGCAG-3' (SEQ ID NO: 12) (atSRp30);

(13) 5'-AAACTAAGCTTAAATATTGAACCGGCCTCGGTTC-3' (SEQ ID NO: 13) (atSRp34/SR1);

(14) 5'-AAACTGGATCCTCTTCCTGTTGGTCGTCGACGATTTG-3' (SEQ ID NO: 14)

(atSRp34/SR1); and

(15) 5'-AAACTGGATCCTCTTCCTTTATCAAATCC-3' (SEQ ID NO: 15)

(atSRp34/SR1)

containing HindIII and BamHI restriction sites. These fragments were digested with HindIII and BamHI and fused to the GUS reporger gene (Jefferson 1987) in pBI101 (Clontech).

Please replace the paragraph beginning on page 21, line 7 with the following amended paragraph:

Expression of atSRp30 and atSRp34/SR1 in bacteria

The coding region of atSRp30 cDNA was amplified by PCR using the primers 5'-ATATACCATGGGTAGCCGATGGAATCGTAC-3' (SEQ ID NO: 16) and (4).

The coding region of atSRp34/SR1 cDNA was amplified by PCR using the primers 5'-ATATACCATGGGCAGTCGT-TCGAG-3' (SEQ ID NO: 17) and (6). The primers contain NcoI and BamHI restriction sites. To obtain the NcoI restriction site, the fourth nucleotide of the coding region in both cases was changed to G. Thus expressed atSRp30 and atSRp34/SR1 have Ser2-Arg and Ser2-Gly substitutions, respectively. The fragments were cloned into the bacterial expression vector pET-3d (Novagen) and transformed into the E. coli strain BL21(DE3)pLysS (Novagen).